RAW SEQUENCE LISTING
PATENT APPLICATION US/09/361,652

DATE: 02/28/2000
TIME: 15:43:47

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This Raw Listing contains the General Information Section and up to first 5 pages.

ENTERED

<110> APPLICANT: Zuker, Charles S.
Adler, Jon Elliot
Lindemeier, Juergen
Ryba, Nick
Hoon, Mark
The Regents of the University of California
<120> TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor Involved in Sensory Transduction
<130> FILE REFERENCE: 02307E-088610US
<140> CURRENT APPLICATION NUMBER: US/09/361,652
<141> CURRENT FILING DATE: 1999-07-27
<150> EARLIER APPLICATION NUMBER: US 60/094,465
<151> EARLIER FILING DATE: 1998-07-28
<160> NUMBER OF SEQ ID NOS: 8
<170> SOFTWARE: PatentIn Ver. 2.1
<210> SEQ ID NO 1
<211> LENGTH: 840
<212> TYPE: PRT
<213> ORGANISM: Rattus sp.
<220> FEATURE:
<223> OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)
<400> SEQUENCE: 1

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Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly Phe Ser
            20                  25                  30
Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His Gly Asp
        35                  40                  45
Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp Arg Pro
    50                  55                  60
Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg Phe
65                  70                  75                  80
Thr Val Glu Glu Ile Asn Asn Ser Ser Ala Leu Leu Pro Asn Ile Thr
                85                  90                  95
Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val Tyr
            100                 105                 110
Ala Thr Leu Arg Val Leu Ala Leu Gln Gly Pro Arg His Ile Glu Ile
        115                 120                 125
Gln Lys Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Phe Ile Gly
    130                 135                 140
Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu Gly Pro
145                 150                 155                 160
Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Val Leu Ser
                165                 170                 175
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45          Ala Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Arg
46                      180                 185                 190
47          His Gln Val Glu Val Met Val Gln Leu Leu Gln Ser Phe Gly Trp Val
48                  195                 200                 205
49          Trp Ile Ser Leu Ile Gly Ser Tyr Gly Asp Tyr Gly Gln Leu Gly Val
50              210                 215                 220
51          Gln Ala Leu Glu Glu Leu Ala Val Pro Arg Gly Ile Cys Val Ala Phe
52          225                 230                 235                 240
53          Lys Asp Ile Val Pro Phe Ser Ala Arg Val Gly Asp Pro Arg Met Gln
54                          245                 250                 255
55          Ser Met Met Gln His Leu Ala Gln Ala Arg Thr Thr Val Val Val Val
56                      260                 265                 270
57          Phe Ser Asn Arg His Leu Ala Arg Val Phe Phe Arg Ser Val Val Leu
58                  275                 280                 285
59          Ala Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Asp Trp Ala Ile
60              290                 295                 300
61          Ser Thr Tyr Ile Thr Ser Val Thr Gly Ile Gln Gly Ile Gly Thr Val
62          305                 310                 315                 320
63          Leu Gly Val Ala Val Gln Gln Arg Gln Val Pro Gly Leu Lys Glu Phe
64                          325                 330                 335
65          Glu Glu Ser Tyr Val Arg Ala Val Thr Ala Ala Pro Ser Ala Cys Pro
66                      340                 345                 350
67          Glu Gly Ser Trp Cys Ser Thr Asn Gln Leu Cys Arg Glu Cys His Thr
68                  355                 360                 365
69          Phe Thr Thr Arg Asn Met Pro Thr Leu Gly Ala Phe Ser Met Ser Ala
70              370                 375                 380
71          Ala Tyr Arg Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly Leu His
72          385                 390                 395                 400
73          Gln Leu Leu Gly Cys Thr Ser Glu Ile Cys Ser Arg Gly Pro Val Tyr
74                          405                 410                 415
75          Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu Leu His
76                      420                 425                 430
77          Glu Asn Thr Val Ala Phe Asp Asp Asn Gly Asp Thr Leu Gly Tyr Tyr
78                  435                 440                 445
79          Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe Glu Ile
80              450                 455                 460
81          Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn Lys Thr
82          465                 470                 475                 480
83          Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser Val Cys
84                          485                 490                 495
85          Thr Thr Asp Cys Leu Ala Gly His His Arg Val Val Val Gly Ser His
86                      500                 505                 510
87          His Cys Cys Phe Glu Cys Val Pro Cys Glu Ala Gly Thr Phe Leu Asn
88                  515                 520                 525
89          Met Ser Glu Leu His Ile Cys Gln Pro Cys Gly Thr Glu Glu Trp Ala
90              530                 535                 540
91          Pro Lys Glu Ser Thr Thr Cys Phe Pro Arg Thr Val Glu Phe Leu Ala
92          545                 550                 555                 560
93          Trp His Glu Pro Ile Ser Leu Val Leu Ile Ala Ala Asn Thr Leu Leu
94                          565                 570                 575
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Leu Leu Leu Leu Val Gly Thr Ala Gly Leu Phe Ala Trp His Phe His
580 585 590
Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu
595 600 605
Gly Ser Leu Val Ala Gly Ser Cys Ser Phe Tyr Ser Phe Phe Gly Glu
610 615 620
Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser Leu Gly
625 630 635 640
Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln Leu Val
645 650 655
Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr Arg Thr Trp
660 665 670
Ala Gln Asn His Gly Ala Gly Leu Phe Val Ile Val Ser Ser Thr Val
675 680 685
His Leu Leu Ile Cys Leu Thr Trp Leu Val Met Trp Thr Pro Arg Pro
690 695 700
Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu Cys Thr
705 710 715 720
Glu Val Asn Ser Val Gly Phe Leu Leu Ala Phe Thr His Asn Ile Leu
725 730 735
Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu Leu Pro
740 745 750
Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Leu Asn
755 760 765
Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ala Ser Ile Tyr Gln Gly
770 775 780
Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Thr Thr Leu Ser
785 790 795 800
Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys
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Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile Gln Asp
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Tyr Thr Arg Arg Cys Gly Thr Thr
835 840

<210> SEQ ID NO 2
<211> LENGTH: 842
<212> TYPE: PRT
<213> ORGANISM: Mus sp.
<220> FEATURE:
<223> OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)
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Phe Ser Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His
35 40 45
Ala Asp Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp
50 55 60
Arg Ser Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met

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145          65                  70                  75                  80
146      Arg Phe Thr Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn
147                      85                  90                  95
148      Ile Thr Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ser Asn
149                  100                 105                 110
150      Val Tyr Ala Thr Leu Arg Val Pro Ala Gln Gln Gly Thr Gly His Leu
151              115                 120                 125
152      Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu
153          130                 135                 140
154      Ile Gly Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu
155      145                 150                 155                 160
156      Ser Pro Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Ile
157                      165                 170                 175
158      Leu Ser Gly Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Ile Pro Ser
159                  180                 185                 190
160      Asp Lys Tyr Gln Val Glu Val Ile Val Arg Leu Leu Gln Ser Phe Gly
161              195                 200                 205
162      Trp Val Trp Ile Ser Leu Val Gly Ser Tyr Gly Asp Tyr Gly Gln Leu
163          210                 215                 220
164      Gly Val Gln Ala Leu Glu Glu Leu Ala Thr Pro Arg Gly Ile Cys Val
165      225                 230                 235                 240
166      Ala Phe Lys Asp Val Val Pro Leu Ser Ala Gln Ala Gly Asp Pro Arg
167                      245                 250                 255
168      Met Gln Arg Met Met Leu Arg Leu Ala Arg Ala Arg Thr Thr Val Val
169                  260                 265                 270
170      Val Val Phe Ser Asn Arg His Leu Ala Gly Val Phe Phe Arg Ser Val
171              275                 280                 285
172      Val Leu Ala Asn Leu Thr Gly Lys Val Trp Ile Ala Ser Glu Asp Trp
173          290                 295                 300
174      Ala Ile Ser Thr Tyr Ile Thr Asn Val Pro Gly Ile Gln Gly Ile Gly
175      305                 310                 315                 320
176      Thr Val Leu Gly Val Ala Ile Gln Gln Arg Gln Val Pro Gly Leu Lys
177                      325                 330                 335
178      Glu Phe Glu Glu Ser Tyr Val Gln Ala Val Met Gly Ala Pro Arg Thr
179                  340                 345                 350
180      Cys Pro Glu Gly Ser Trp Cys Gly Thr Asn Gln Leu Cys Arg Glu Cys
181              355                 360                 365
182      His Ala Phe Thr Thr Trp Asn Met Pro Glu Leu Gly Ala Phe Ser Met
183          370                 375                 380
184      Ser Ala Ala Tyr Asn Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly
185      385                 390                 395                 400
186      Leu His Gln Leu Leu Gly Cys Thr Ser Gly Thr Cys Ala Arg Gly Pro
187                      405                 410                 415
188      Val Tyr Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu
189                  420                 425                 430
190      Leu His Lys Lys Thr Val Ala Phe Asp Asp Lys Gly Asp Pro Leu Gly
191              435                 440                 445
192      Tyr Tyr Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe
193          450                 455                 460
194      Glu Val Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn
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195          465                 470                 475                 480
196          Lys Thr Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser
197                              485                 490                 495
198          Val Cys Thr Arg Asp Cys Leu Glu Gly His His Arg Leu Val Met Gly
199                          500                 505                 510
200          Ser His His Cys Cys Phe Glu Cys Met Pro Cys Glu Ala Gly Thr Phe
201                      515                 520                 525
202          Leu Asn Thr Ser Glu Leu His Thr Cys Gln Pro Cys Gly Thr Glu Glu
203                  530                 535                 540
204          Trp Ala Pro Glu Gly Ser Ser Ala Cys Phe Ser Arg Thr Val Glu Phe
205          545                 550                 555                 560
206          Leu Gly Trp His Glu Pro Ile Ser Leu Val Leu Leu Ala Ala Asn Thr
207                              565                 570                 575
208          Leu Leu Leu Leu Leu Leu Ile Gly Thr Ala Gly Leu Phe Ala Trp Arg
209                          580                 585                 590
210          Leu His Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu
211                      595                 600                 605
212          Met Leu Gly Ser Leu Val Ala Gly Ser Cys Ser Leu Tyr Ser Phe Phe
213                  610                 615                 620
214          Gly Lys Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser
215          625                 630                 635                 640
216          Leu Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln
217                              645                 650                 655
218          Leu Val Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His
219                          660                 665                 670
220          Thr Trp Ala Gln Asn His Gly Ala Gly Ile Phe Val Ile Val Ser Ser
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224          Arg Pro Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu
225          705                 710                 715                 720
226          Cys Thr Glu Val Asn Ser Val Gly Phe Leu Val Ala Phe Ala His Asn
227                              725                 730                 735
228          Ile Leu Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu
229                          740                 745                 750
230          Leu Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu
231                      755                 760                 765
232          Leu His Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ser Ser Ile Tyr
233                  770                 775                 780
234          Gln Gly Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Ala Thr
235          785                 790                 795                 800
236          Leu Ser Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile
237                              805                 810                 815
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242      <210> SEQ ID NO 3
243      <211> LENGTH: 777
244      <212> TYPE: PRT
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VERIFICATION SUMMARY
PATENT APPLICATION **US/09/361,652**

DATE: 02/28/2000
TIME: 15:43:47

Input Set: **I361652.RAW**

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Application No.: 09/361,652

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- [X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- [X] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- [X] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- [ ] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- [ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- [ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- [ ] 7. Other: _____

Applicant Must Provide:

- [X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- [X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- [X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

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